

SEQUENCE LISTING

Q1
(1) GENERAL INFORMATION:

5 (i) APPLICANT: Ashkenazi, Avi J.
Baker, Kevin
Gurney, Austin
Wood, William

10 (ii) TITLE OF INVENTION: Apo-2DcR

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Genentech, Inc.
20 (B) STREET: 460 Point San Bruno Blvd
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

30 (A) APPLICATION NUMBER:
(B) FILING DATE: 18-Jun-1997
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

35 (A) NAME: Marschang, Diane L.
(B) REGISTRATION NUMBER: 35,600

(C) REFERENCE/DOCKET NUMBER: P1110

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415/225-5416

(B) TELEFAX: 415/952-9881

(C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile Val
1 5 10 15

Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg
20 25 30

Gln Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg
35 40 45

His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser
50 55 60

Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr
65 70 75

Thr Asn Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val
80 85 90

Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg

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	Asp	Thr	Val	Cys	Gln	Cys	Lys	Glu	Gly	Thr	Phe	Arg	Asn	Glu	Asn
					110					115				120	
5	Ser	Pro	Glu	Met	Cys	Arg	Lys	Cys	Ser	Arg	Cys	Pro	Ser	Gly	Glu
					125					130				135	
	Val	Gln	Val	Ser	Asn	Cys	Thr	Ser	Trp	Asp	Asp	Ile	Gln	Cys	Val
10					140					145				150	
	Glu	Glu	Phe	Gly	Ala	Asn	Ala	Thr	Val	Glu	Thr	Pro	Ala	Ala	Glu
					155					160				165	
	Glu	Thr	Met	Asn	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu
					170					175				180	
	Glu	Thr	Met	Asn	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu
					185					190				195	
	Glu	Thr	Met	Thr	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu
					200					205				210	
	Glu	Thr	Met	Thr	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu
					215					220				225	
	Glu	Thr	Met	Thr	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Ser	Ser	His	Tyr
					230					235				240	
30	Leu	Ser	Cys	Thr	Ile	Val	Gly	Ile	Ile	Val	Leu	Ile	Val	Leu	Leu
					245					250				255	
	Ile	Val	Phe	Val											
					259										

a₁ (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1180 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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GCTGTGGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG 50

ATTTTGGGA GTTTGACCAG AGATGCAAGG GGTGAAGGAG CGCTTCCTAC 100

CGTTAGGGAA CTCTGGGGAC AGAGCGCCCC GGCCGCCTGA TGGCCGAGGC 150

AGGGTGCGAC CCAGGACCCA GGACGGCGTC GGGAACCATA CC ATG 195

Met

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GCC CGG ATC CCC AAG ACC CTA AAG TTC GTC GTC GTC ATC 234

Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile

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GTC GCG GTC CTG CTG CCA GTC CTA GCT TAC TCT GCC ACC 273

Val Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr

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30 ACT GCC CGG CAG GAG GAA GTT CCC CAG CAG ACA GTG GCC 312

Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala

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CCA CAG CAA CAG AGG CAC AGC TTC AAG GGG GAG GAG TGT 351

35 Pro Gln Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys

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CCA GCA GGA TCT CAT AGA TCA GAA CAT ACT GGA GCC TGT 390
Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala Cys

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AAC CCG TGC ACA GAG GGT GTG GAT TAC ACC AAC GCT TCC 429
Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser

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AAC AAT GAA CCT TCT TGC TTC CCA TGT ACA GTT TGT AAA 468
Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys

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TCA GAT CAA AAA CAT AAA AGT TCC TGC ACC ATG ACC AGA 507
Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg

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105

GAC ACA GTG TGT CAG TGT AAA GAA GGC ACC TTC CGG AAT 546
Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn

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GAA AAC TCC CCA GAG ATG TGC CGG AAG TGT AGC AGG TGC 585
Glu Asn Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys

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125

130

CCT AGT GGG GAA GTC CAA GTC AGT AAT TGT ACG TCC TGG 624
Pro Ser Gly Glu Val Gln Val Ser Asn Cys Thr Ser Trp

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GAT GAT ATC CAG TGT GTT GAA GAA TTT GGT GCC AAT GCC 663
Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala Asn Ala

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ACT GTG GAA ACC CCA GCT GCT GAA GAG ACA ATG AAC ACC 702

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Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr
160 165 170

5 AGC CCG GGG ACT CCT GCC CCA GCT GCT GAA GAG ACA ATG 741
Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met
175 180

10 AAC ACC AGC CCA GGG ACT CCT GCC CCA GCT GCT GAA GAG 780
Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu
185 190 195

ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC CCA GCT GCT 819
Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala
200 205

GAA GAG ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC CCA 858
Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro
210 215 220

GCT GCT GAA GAG ACA ATG ACC ACC AGC CCG GGG ACT CCT 897
Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro
225 230 235

GCC TCT TCT CAT TAC CTC TCA TGC ACC ATC GTA GGG ATC 936
Ala Ser Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile
240 245

ATA GTT CTA ATT GTG CTT CTG ATT GTG TTT GTT T 970
Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
250 255 259

GAAAGACTTC ACTGTGGAAG AAATTCCTTC CTTACCTGAA AGGTTTCAGGT 1020

AGGCGCTGGC TGAGGGCGGG GGGCGCTGGA CACTCTCTGC CCTGCCTCCC 1070

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TCTGCTGTGT TCCCACAGAC AGAAACGCCT GCCCCTGCCC CAAAAAAAAA 1120

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1170

5 AAAAAAAAAA 1180

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 299 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly
-40 -35 -30

Asp Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro
-25 -20 -15

Arg Thr Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro
-10 -5 1 5

Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro
10 15 20

Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro
25 30 35

Gln Gln Thr Val Ala Pro Gln Gln Gln Arg His Ser Phe Lys Gly
40 45 50

Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala
55 60 65

21 Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn
 70 75 80
 Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln
 5 85 90 95
 Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln
 100 105 110
 Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro Glu Met Cys
 115 120 125
 Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu Val Gln Val Ser Asn
 130 135 140
 Cys Thr Ser Trp Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala
 145 150 155
 Asn Ala Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr
 160 165 170
 Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Asn Thr
 175 180 185
 Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
 190 195 200
 Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
 205 210 215
 Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
 220 225 230
 Ser Pro Gly Thr Pro Ala Ser Ser His Tyr Leu Ser Cys Thr Ile
 235 240 245

a1 Val Gly Ile Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
250 255 259

(2) INFORMATION FOR SEQ ID NO:4:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1180 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

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(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCTGTGGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG 50

ATTTTTGGGA GTTTGACCAG AG ATG CAA GGG GTG AAG GAG 90

Met Gln Gly Val Lys Glu

-40

-35

CGC TTC CTA CCG TTA GGG AAC TCT GGG GAC AGA GCG CCC 129

Arg Phe Leu Pro Leu Gly Asn Ser Gly Asp Arg Ala Pro

-30

-25

CGG CCG CCT GAT GGC CGA GGC AGG GTG CGA CCC AGG ACC 168

Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro Arg Thr

-20

-15

-10

CAG GAC GGC GTC GGG AAC CAT ACC ATG GCC CGG ATC CCC 207

Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro

-5

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AAG ACC CTA AAG TTC GTC GTC GTC ATC GTC GCG GTC CTG 246

Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu

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01 CTG CCA GTC CTA GCT TAC TCT GCC ACC ACT GCC CGG CAG 285
 Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln
 20 25 30

5 GAG GAA GTT CCC CAG CAG ACA GTG GCC CCA CAG CAA CAG 324
 Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln
 35 40

10 AGG CAC AGC TTC AAG GGG GAG GAG TGT CCA GCA GGA TCT 363
 Arg His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser
 45 50 55

CAT AGA TCA GAA CAT ACT GGA GCC TGT AAC CCG TGC ACA 402
 His Arg Ser Glu His Thr Gly Ala Cys Asn Pro Cys Thr
 60 65 70

GAG GGT GTG GAT TAC ACC AAC GCT TCC AAC AAT GAA CCT 441
 Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn Asn Glu Pro
 75 80

TCT TGC TTC CCA TGT ACA GTT TGT AAA TCA GAT CAA AAA 480
 Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln Lys
 85 90 95

25 CAT AAA AGT TCC TGC ACC ATG ACC AGA GAC ACA GTG TGT 519
 His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys
 100 105

30 CAG TGT AAA GAA GGC ACC TTC CGG AAT GAA AAC TCC CCA 558
 Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro
 110 115 120

35 GAG ATG TGC CGG AAG TGT AGC AGG TGC CCT AGT GGG GAA 597
 Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu
 125 130 135

31

GTC CAA GTC AGT AAT TGT ACG TCC TGG GAT GAT ATC CAG 636
Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln
140 145

5 TGT GTT GAA GAA TTT GGT GCC AAT GCC ACT GTG GAA ACC 675
Cys Val Glu Glu Phe Gly Ala Asn Ala Thr Val Glu Thr
150 155 160

10 CCA GCT GCT GAA GAG ACA ATG AAC ACC AGC CCG GGG ACT 714
Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr
165 170

CCT GCC CCA GCT GCT GAA GAG ACA ATG AAC ACC AGC CCA 753
Pro Ala Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro
175 180 185

GGG ACT CCT GCC CCA GCT GCT GAA GAG ACA ATG ACC ACC 792
Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
190 195 200

AGC CCG GGG ACT CCT GCC CCA GCT GCT GAA GAG ACA ATG 831
Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met
205 210

ACC ACC AGC CCG GGG ACT CCT GCC CCA GCT GCT GAA GAG 870
Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu
215 220 225

30 ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC TCT TCT CAT 909
Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His
230 235

35 TAC CTC TCA TGC ACC ATC GTA GGG ATC ATA GTT CTA ATT 948
Tyr Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile
240 245 250

Q1 GTG CTT CTG ATT GTG TTT GTT T GAAAGACTTC ACTGTGGAAG 990
Val Leu Leu Ile Val Phe Val
255 259

5 AAATTCCTTC CTTACCTGAA AGGTTTCAGGT AGGCGCTGGC TGAGGGCGGG 1040
GGGCGCTGGA CACTCTCTGC CCTGCCTCCC TCTGCTGTGT TCCCACAGAC 1090
AGAAACGCCT GCCCCTGCCC CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1140
10 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1180

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGTAAAACGA CGGCCAGTTA AATAGACCTG CAATTATTAA TCT 43

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

a | CAGGAAACAG CTATGACCAC CTGCACACCT GCAAATCCAT T 41

(2) INFORMATION FOR SEQ ID NO:7:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His
1 5 10 15
Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly
20 25 30
Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys
35 40 45
Gly Cys Arg Lys
49

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn
1 5 10 15

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Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln
20 25 30

Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln
5 35 40 45

Cys Lys Glu
48

10 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGAGCCGCT CATGAGGAAG TTGGGCCTCA TGGACAATGA GATAAAGGTG 50

GCTAAAGCTG AGGCAGCGGG 70

25 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1799 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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CCCACGCGTC CGCATAAATC AGCACGCGGC CGGAGAACCC CGCAATCTCT 50

GCGCCACAA AATACACCGA CGATGCCCCGA TCTACTTTAA GGGCTGAAAC 100

5 CCACGGGCCT GAGAGACTAT AAGAGCGTTC CCTACCGCC ATG GAA 145
Met Glu
1

10 CAA CGG GGA CAG AAC GCC CCG GCC GCT TCG GGG GCC CGG 184
Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
5 10 15

AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA GCC 223
Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala
20 25

AGG CCT GGG CTC CGG GTC CCC AAG ACC CTT GTG CTC GTT 262
Arg Pro Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val
30 35 40

GTC GCC GCG GTC CTG CTG TTG GTC TCA GCT GAG TCT GCT 301
Val Ala Ala Val Leu Leu Leu Val Ser Ala Glu Ser Ala
45 50

25 CTG ATC ACC CAA CAA GAC CTA GCT CCC CAG CAG AGA GCG 340
Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln Gln Arg Ala
55 60 65

30 GCC CCA CAA CAA AAG AGG TCC AGC CCC TCA GAG GGA TTG 379
Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
70 75 80

35 TGT CCA CCT GGA CAC CAT ATC TCA GAA GAC GGT AGA GAT 418
Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp
85 90

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T06TTT-20

21 TGC ATC TCC TGC AAA TAT GGA CAG GAC TAT AGC ACT CAC 457
 Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His
 95 100 105

5 TGG AAT GAC CTC CTT TTC TGC TTG CGC TGC ACC AGG TGT 496
 Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys
 110 115

10 GAT TCA GGT GAA GTG GAG CTA AGT CCC TGC ACC ACG ACC 535
 Asp Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr
 120 125 130

AGA AAC ACA GTG TGT CAG TGC GAA GAA GGC ACC TTC CGG 574
 Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe Arg
 135 140 145

GAA GAA GAT TCT CCT GAG ATG TGC CGG AAG TGC CGC ACA 613
 Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr
 150 155

GGG TGT CCC AGA GGG ATG GTC AAG GTC GGT GAT TGT ACA 652
 Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr
 160 165 170

25 CCC TGG AGT GAC ATC GAA TGT GTC CAC AAA GAA TCA GGC 691
 Pro Trp Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly
 175 180

30 ATC ATC ATA GGA GTC ACA GTT GCA GCC GTA GTC TTG ATT 730
 Ile Ile Ile Gly Val Thr Val Ala Ala Val Val Leu Ile
 185 190 195

35 GTG GCT GTG TTT GTT TGC AAG TCT TTA CTG TGG AAG AAA 769
 Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys
 200 205 210

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 GTC CTT CCT TAC CTG AAA GGC ATC TGC TCA GGT GGT GGT 808
 Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly
 215 220

5 GGG GAC CCT GAG CGT GTG GAC AGA AGC TCA CAA CGA CCT 847
 Gly Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro
 225 230 235

10 GGG GCT GAG GAC AAT GTC CTC AAT GAG ATC GTG AGT ATC 886
 Gly Ala Glu Asp Asn Val Leu Asn Glu Ile Val Ser Ile
 240 245

TTG CAG CCC ACC CAG GTC CCT GAG CAG GAA ATG GAA GTC 925
 Leu Gln Pro Thr Gln Val Pro Glu Gln Glu Met Glu Val
 250 255 260

CAG GAG CCA GCA GAG CCA ACA GGT GTC AAC ATG TTG TCC 964
 Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser
 265 270 275

CCC GGG GAG TCA GAG CAT CTG CTG GAA CCG GCA GAA GCT 1003
 Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
 280 285

25 GAA AGG TCT CAG AGG AGG AGG CTG CTG GTT CCA GCA AAT 1042
 Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn
 290 295 300

30 GAA GGT GAT CCC ACT GAG ACT CTG AGA CAG TGC TTC GAT 1081
 Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp
 305 310

35 GAC TTT GCA GAC TTG GTG CCC TTT GAC TCC TGG GAG CCG 1120
 Asp Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro
 315 320 325

21 CTC ATG AGG AAG TTG GGC CTC ATG GAC AAT GAG ATA AAG 1159
 Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile Lys
 330 335 340

5 GTG GCT AAA GCT GAG GCA GCG GGC CAC AGG GAC ACC TTG 1198
 Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu
 345 350

10 TAC ACG ATG CTG ATA AAG TGG GTC AAC AAA ACC GGG CGA 1237
 Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg
 355 360 365

GAT GCC TCT GTC CAC ACC CTG CTG GAT GCC TTG GAG ACG 1276
 Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr
 370 375

CTG GGA GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC 1315
 Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His
 380 385 390

TTG TTG AGC TCT GGA AAG TTC ATG TAT CTA GAA GGT AAT 1354
 Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
 395 400 405

25 GCA GAC TCT GCC WTG TCC TAAGTGTG ATTCTCTTCA GGAAGTGAGA 1400
 Ala Asp Ser Ala Xaa Ser
 410 411

30 CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC 1450
 AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC 1500
 CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACTT TTTACTGCAC 1550

35 TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT 1600

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GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTGTT TGGGATGTCA 1650

TTGTTTTTAC AGCACTTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT 1700

5 TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAAA AAAAAAAG 1750

GGCGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC 1799

(2) INFORMATION FOR SEQ ID NO:11:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
1 5 10 15

Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro
20 25 30

Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val
35 40 45

Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp
50 55 60

Leu Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser
65 70 75

Pro Ser Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp
80 85 90

35

21 Gly Arg Asp Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr
 95 100 105

 5 His Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp
 110 115 120

 Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr Arg Asn Thr
 125 130 135

 10 Val Cys Gln Cys Glu Glu Gly Thr Phe Arg Glu Glu Asp Ser Pro
 140 145 150

 Glu Met Cys Arg Lys Cys Arg Thr Gly Cys Pro Arg Gly Met Val
 155 160 165

 Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile Glu Cys Val His
 170 175 180

 Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val
 185 190 195

 20 Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys
 200 205 210

 25 Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly Asp
 215 220 225

 Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
 230 235 240

 30 Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val
 245 250 255

 Pro Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly
 260 265 270

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21 Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro
 275 280 285
 5 Ala Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala
 290 295 300
 Asn Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp
 305 310 315
 10 Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg
 320 325 330
 Lys Leu Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu
 335 340 345
 Ala Ala Gly His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp
 350 355 360
 Val Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp
 365 370 375
 Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu
 380 385 390
 25 Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
 395 400 405
 Ala Asp Ser Ala Xaa Ser
 410 411

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(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: Nucleic Acid

35

B1

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

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ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:13:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

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AGGATGGGAA GTGTGTGATA TATCCTTGAT 30

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